

Figure 1A

>775133	GGNCAGAGCC	TGCGCAGGGC	AGGAGCAGCT	GGCCCACTGG	CGGCCCCGCAA
>1338704	AGAGCC	TGCGCAGGGC	AGGAGCAGCT	GGCCCACTGG	CGGCCCCGCAA
>2645837				TGG	CGGCCCCGCAA
Consensus	GGNCAGAGCC	TGCGCAGGGC	AGGAGCAGCT	GGCCCACTGG	CGGCCCCGCAA
>775133	CACTNCGTCT	TNACCCTCTG	GGCCCACTGC	ATCTAGAGGA	GGGCCGTCTG
>1338704	CACTCCGTCT	:CACCCTCTG	GGCNCACCTGC	ATCTAGAGGA	GGGCCGTCTG
>2645837	CACTCCGTCT	:CACCCTCTG	GGCCCACTGC	ATCTAGAGGA	GGGCCGTCTG
>775762		CCCTCTG	GGCCCACTGC	ATCTAGAGGA	GGGCCGTCTG
>3210629				CACGA	GGGCCGTCTG
Consensus	CACTCCGTCT	:CACCCTCTG	GGCCCACTGC	ATCTAGAGGA	GGGCCGTCTG
>775133	TGAGGCCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGAAGCTGG
>1338704	TNAGGCCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGANGCTGG
>2645837	TGAGGNCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGAATCTGG
>775762	TGAGGCCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGAAGCTGG
>3210629	TNAGGCCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGANGCTGG
Consensus	TGAGGCCACT	ACCCCTCCAG	CAACTGGGAG	GTGGGACTGT	CAGAAGCTGG
>775133	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
>1338704	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
>2645837	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
>775762	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
>3210629	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
Consensus	CCCAGGGTGG	TGGTCAGCTG	GGTCAGGGAC	CTACGGCACC	TGCTGGACCA
>775133	NCTNGNCTTT	TCCATCGAAG	CAGGGAAGTG	GGAGCCTTGA	GCCCTTGCGGT
>1338704	CCTCGCCTTC	TCCATCGAAG	CAGGGAANTG	GGAGCCTCGA	GCCCTCGCGGT
>2645837	CCTCGCCTTC	TCCATCGAAG	CAGGGAAGTG	GGAGCCTCGA	GCCCTCGCGGT
>775762	CCTCGCCTTC	TCCATCGAAG	CAGGGAAGTG	GGAGCCTCGA	GCCCTCGCGGT
>3210629	CCTCGCCTTC	TCCATCGAAG	CAGGGAAGTG	GGAGCCTCGA	GCCCTCGCGGT
Consensus	CCTCGCCTTC	TCCATCGAAG	CAGGGAAGTG	GGAGCCTCGA	GCCCTCGCGGT
>775133	GGAAGCTTGA	CCCCAAGCCA	CTT		
>1338704	GGAAG				
>2645837	GGAAGCT:GA	CCCCAAGCCA	NNCTTCACCT	GGACAGGAT	
>775762	GGAAGCT:GA	CCCCAAGCCA	CCCTTCACCT	GGACAGGATG	AGAGTGT
>3210629	GGAAGCT:GA	CCCCAAGCCA	CCCTTCACNT	GGACAGGATG	AGAGTGTGAC
Consensus	GGAAGCT:GA	CCCCAAGCCA	CCCTTCACCT	GGACAGGATG	AGAGTGTGAC
>3210629	GTGTGCTTCG	CCTCCTGGCC	CTCATCTTTG	CCATAGTCAC	GACATGGATG
>1281865					GATG
>1281865					GATG
Consensus	GTGTGCTTCG	CCTCCTGGCC	CTCATCTTTG	CCATAGTCAC	GACATGGATG
>3210629	TTTATTCGAA	GCTACATGAG	CTT		
>1281865	TTTATTCGAA	GCTACATGAG	CTTCAGCATG	AAAACCATCC	GTCTGCCACG
>1281865	TTTATTCGAA	GCTACATGAG	CTTCAGCATG	AAAACCATCC	GTCTGCCACG
Consensus	TTTATTCGAA	GCTACATGAG	CTTCAGCATG	AAAACCATCC	GTCTGCCACG

Figure 1B

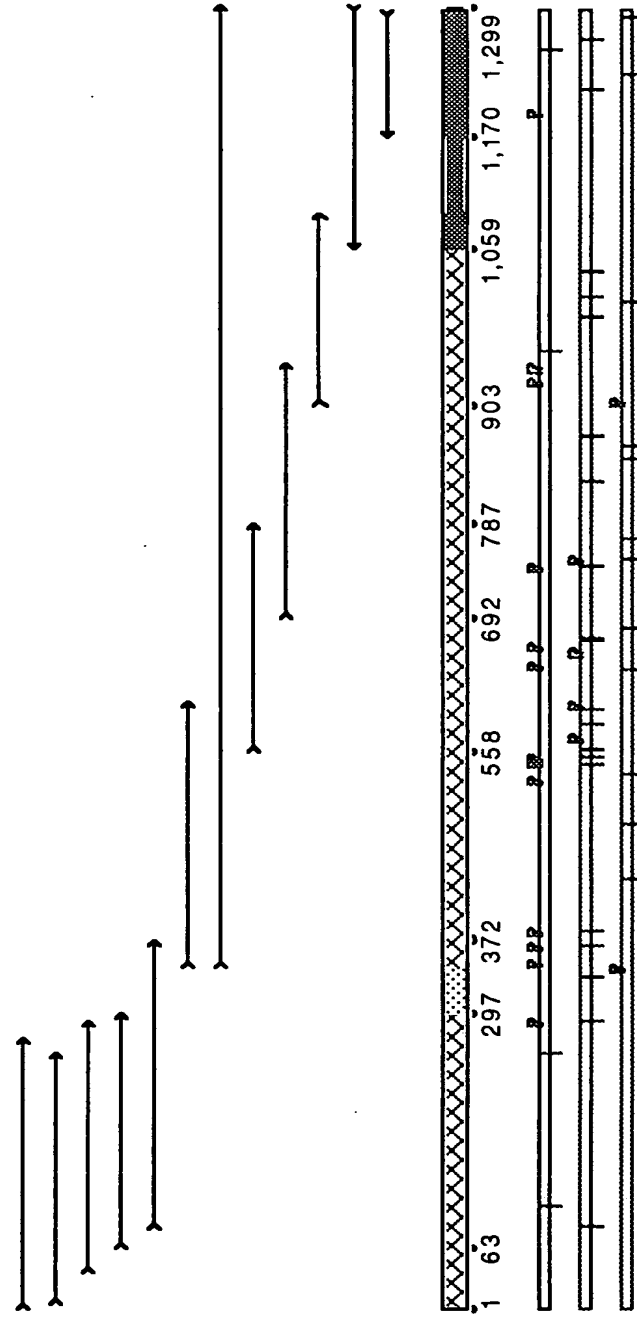
>1281865	CTGGCTGGCC	TCGCCCACCA	AGGAGATCCA	GGTTAAAAAG	TACAAGTGTG
>1281865	CTGGCTGGCC	TCGCCCACCA	AGGAGATCCA	GGTTAAAAAG	TACAAGTGTG
Consensus	CTGGCTGGCC	TCGCCCACCA	AGGAGATCCA	GGTTAAAAAG	TACAAGTGTG
>1281865	GCCTCATCAA	GCCCTGCCCC	GCCAACTACT	TTGCGTTTAA	AATCTGCAGT
>1281865	GCCTCATCAA	GCCCTGCCCC	GCCAACTACT	TTGCGTTTAA	AATCTGCAGT
Consensus	GCCTCATCAA	GCCCTGCCCC	GCCAACTACT	TTGCGTTTAA	AATCTGCAGT
>1281865	GGGGCCGCCA	ACGTCGTGGG	CCCTACTATG	TGCTTTGAAG	ACCGCATGAT
>1281865	GGGGCCGCCA	ACGTCGTGGG	CCCTACTATG	TGCTTTGAAG	ACCGCATGAT
Consensus	GGGGCCGCCA	ACGTCGTGGG	CCCTACTATG	TGCTTTGAAG	ACCGCATGAT
>1281865	CATGAGTCCT	GTGAAAAACA	ATGTGGGCAG	AGGCCTAAAC	ATCGCCCTGG
>1281865	CATGAGTCCT	GTGAAAAACA	ATGTGGGCAG	AGGCCTAAAC	ATCGCCCTGG
>1807758		GTGAAAAACA	ATGTGGGCAG	AGGCCTAAAC	ATCGCCCTGG
Consensus	CATGAGTCCT	GTGAAAAACA	ATGTGGGCAG	AGGCCTAAAC	ATCGCCCTGG
>1281865	TGAATGGAA				
>1281865	TGAATGGAAC	CACGGGAGCT	GTGCTGGGAC	AGAAGGCATT	TGACATGTAC
>1807758	TGAATGGAAC	CACGGGAGCT	GTGCTGGGAC	AGAAGGCATT	TGACATGTAC
Consensus	TGAATGGAAC	CACGGGAGCT	GTGCTGGGAC	AGAAGGCATT	TGACATGTAC
>1281865	TCTGGAGATG	TTATGCACCT	AGTGAAATTC	CTTAAAGAAA	TTCCGGGGGG
>1807758	TCTGGAGATG	TTATGCACCT	AGTGAAATTC	CTTAAAGAAA	TTCCGGGGGG
>1735382					GGGGGG
Consensus	TCTGGAGATG	TTATGCACCT	AGTGAAATTC	CTTAAAGAAA	TTCCGGGGGG
>1281865	TGCACTGGTG	CTGGTGGCCT	CCTACGACGA	TCCAGGGACC	AAAATGAACG
>1807758	TGCACTGGTG	CTGGTGGCCT	CCTACGACGA	TCCAGGGACC	AAAATGAACG
>1735382	TGCACTGGTG	CTGGTGGCCT	CCTACGACGA	TCCAGGGACC	AAAATGAACG
Consensus	TGCACTGGTG	CTGGTGGCCT	CCTACGACGA	TCCAGGGACC	AAAATGAACG
>1281865	ATGAAAGCAG	GAAACTCTTC	TCTGACTTGG	GGAGTTCCTA	CGCAAAACAA
>1807758	ATGAAAGCAG	GAAACTCTTC	TCTGACTTGG	GGAGTTCCTA	
>1735382	ATGAAAGCAG	GAAACTCTTC	TCTGACTTGG	GGAGTTCCTA	CGCAAAACAA
Consensus	ATGAAAGCAG	GAAACTCTTC	TCTGACTTGG	GGAGTTCCTA	CGCAAAACAA
>1281865	CTGGGCTTCC	GGGACAGCTG	GGTCTTCATA	GGAGCCAAAG	ACCTCAGGGG
>1735382	CTGGGCTTCC	GGGACAGCTG	GGTCTTCATA	GGAGCCAAAG	ACCTCAGGGG
Consensus	CTGGGCTTCC	GGGACAGCTG	GGTCTTCATA	GGAGCCAAAG	ACCTCAGGGG
>1281865	TAAAAGCCCC	TTTGAGCAGT	TCTTAAAGAA	CAGCCCAGAC	ACAAACAAAT
>1735382	TAAAAGCCCC	TTTGAGCAGT	TCTTAAAGAA	CAGCCCAGAC	ACAAACAAAT
Consensus	TAAAAGCCCC	TTTGAGCAGT	TCTTAAAGAA	CAGCCCAGAC	ACAAACAAAT
>1281865	ACGAGGGATG	GCCAGAGCTG	CTGGAGATGG	AGGGCTGCAT	GCCCCGAAG
>1735382	ACGAGGGATG	GCCAGAGCTG	CTGGAGATGG	AGGGCTGCAT	GCCCC
>2128334	GGGATG	GCCAGAGCTG	CTGGAGATGG	AGGGCTGCAT	GCCCCGAAG
Consensus	ACGAGGGATG	GCCAGAGCTG	CTGGAGATGG	AGGGCTGCAT	GCCCCGAAG

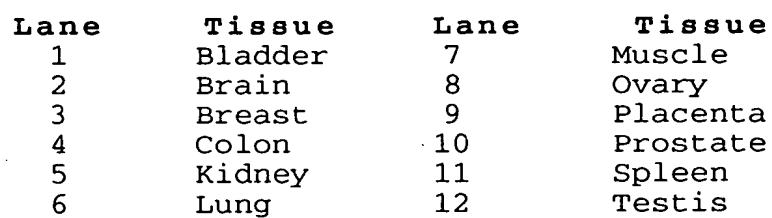
Figure 1C

>1281865	CCATTTTAGG	GTGGCTGTGG	CTCTTCCTCA	GCCAGGGGCC	TGAAGAAGCT
>2128334	CCATTTTAGG	GTGGCTGTGG	CTCTTCCTCA	GCCAGGGGCC	TGAAGAAGCT
Consensus	CCATTTTAGG	GTGGCTGTGG	CTCTTCCTCA	GCCAGGGGCC	TGAAGAAGCT
>1281865	CCTGCCTGAC	TTAGGAGTCA	GAGCCCCGCA	GGGGCTGAGG	AGGAGGAGCA
>2128334	CCTGCCTGAC	TTAGGAGTCA	GAGCCCCGCA	GGGGCTGAGG	AGGAGGAGCA
Consensus	CCTGCCTGAC	TTAGGAGTCA	GAGCCCCGCA	GGGGCTGAGG	AGGAGGAGCA
>1281865	GGGGGTGCTG	CGTGGAAGGT	GCTGCAGGTC	CTTGACACGCT	GTGTCGCGCC
>2128334	GNGGGTGCTG	CGTGGAAGGT	GCTGCAAGTC	CTTGAAAGNN	G
<g2197992		GTGGAAGGT	GCTGCAGGTC	CTTGACACGCT	GTGTCGCGCC
Consensus	GGGGGTGCTG	CGTGGAAGGT	GCTGCAGGTC	CTTGACACGCT	GTGTCGCGCC
>1281865	TCTCCTCCTC	GGAAACAGAA	CCCTCCCACA	GCACATCCTA	CCCGGAAGAC
<g2197992	TCTCCTCCTC	GGAAACAGAA	CCCTCCCACA	GCACATCCTA	CCCGGAAGAC
Consensus	TCTCCTCCTC	GGAAACAGAA	CCCTCCCACA	GCACATCCTA	CCCGGAAGAC
>1281865	CAGCCTCAGA	GGGTCCTTCT	GGAACCAGCT	GTCTGTGGAG	AGAATGGGGT
<g2197992	CAGCCTCAGA	GGGTCCTTCT	GGAACCAGCT	GTCTGTGGAG	AGAATGGGGT
<g2409650			AACCAGCT	GTCTGTGGAG	AGAATGGGGT
Consensus	CAGCCTCAGA	GGGTCCTTCT	GGAACCAGCT	GTCTGTGGAG	AGAATGGGGT
>1281865	GCTTTCGTCA	GGGACTGCTG	ACGGCTGGTC	CTGAGGAAGG	ACAAACTGCC
<g2197992	GCTTTCGTCA	GGGACTGCTG	ACGGCTGGTC	CTGAGGAAGG	ACAAACTGCC
<g2409650	GCTTTCGTCA	GGGACTGCTG	ACGGCTGGTC	CTGAGGAAGG	ACAAACTGCC
Consensus	GCTTTCGTCA	GGGACTGCTG	ACGGCTGGTC	CTGAGGAAGG	ACAAACTGCC
>1281865	CAGACTTGAG	CCCAATTAAA	TTTTATTTTT	GCTGGTAAAA	AMAAAWAAMM
<g2197992	CAGACTTGAG	CCCAATTAAA	TTTTATTTTT	GCTGGTTTTG	AAAAAAAAAA
<g2409650	CAGACTTGAG	CCCAATTAAA	TTTTATTTTT	GCTGGTTTTG	AAAAA
Consensus	CAGACTTGAG	CCCAATTAAA	TTTTATTTTT	GCTGGTTTTG	AAAAAAAAAA
>1281865	A				
<g2197992	A				
Consensus	A				

775133
1338704
2645837
775762
3210629
1281865
1281865 IH
1807758
1735382
2128334
92197992
92409650

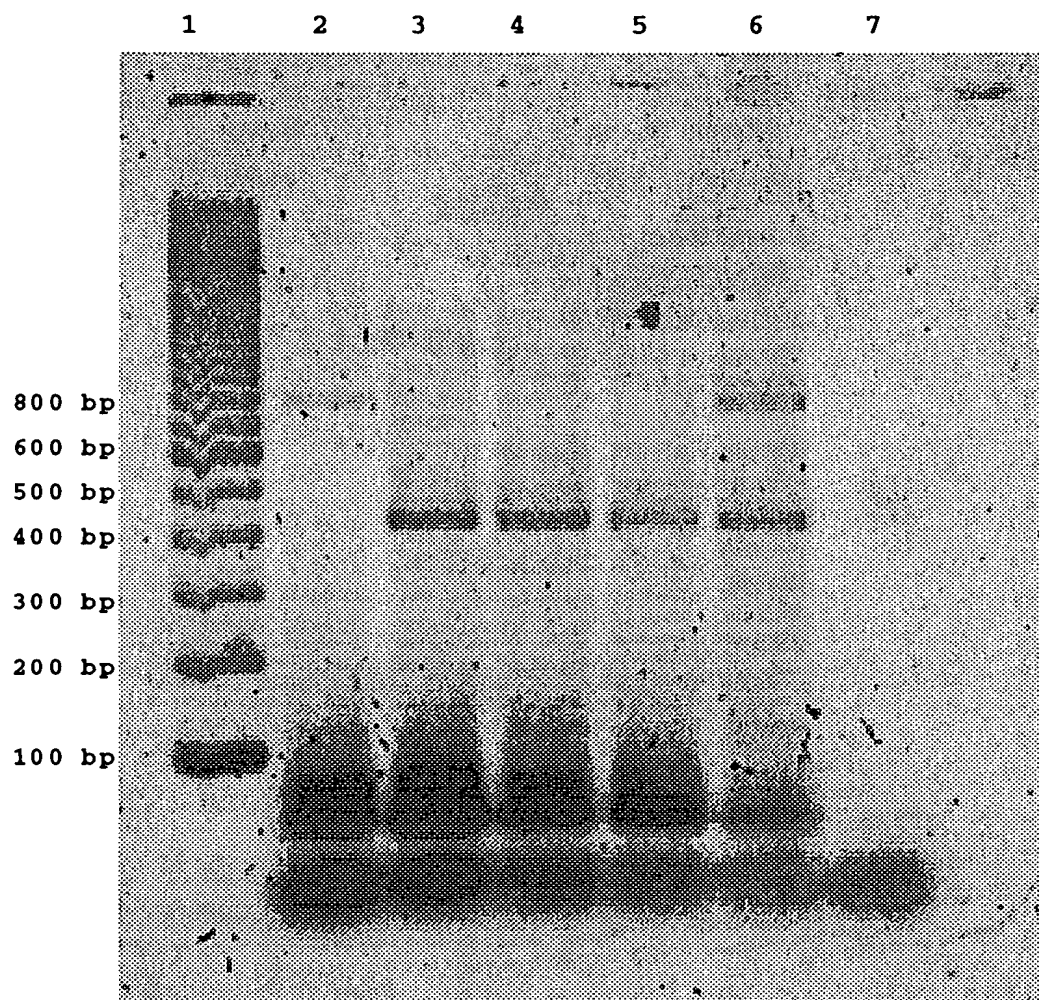
Figure 2



[illegible]

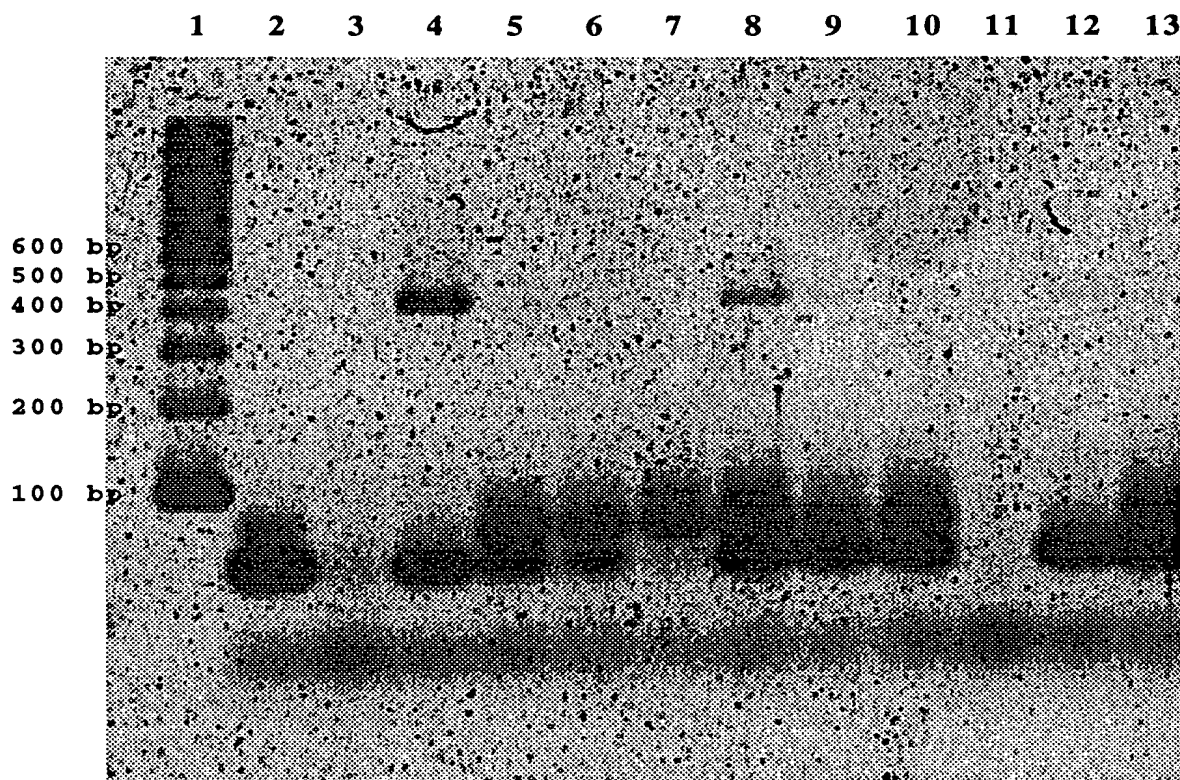
Lane	Tissue	Lane	Tissue
1	Normal Colon	7	Cancer Colon
2	Normal Colon	8	Cancer Colon
3	Normal Colon	9	Cancer Colon
4	Normal Colon	10	Cancer Colon
5	Normal Colon	11	Cancer Colon
6	Normal Colon	12	Cancer Colon

Figure 4A



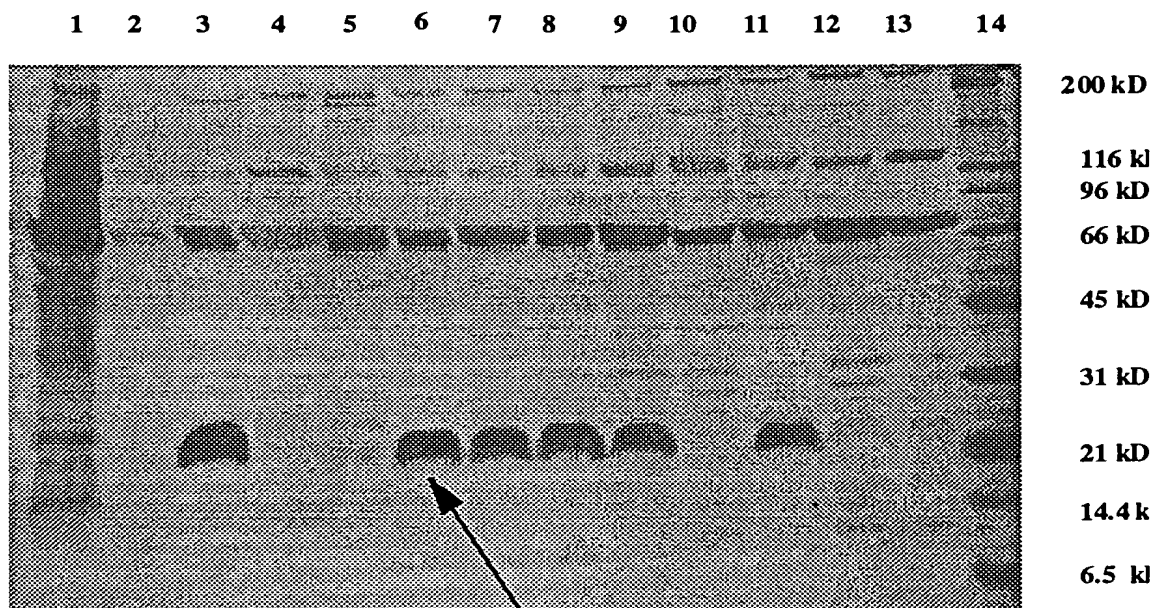
Lane	Tissue
1	DNA Molecular Weight Marker
2	Normal Colon
3	Cancer Colon
4	Cancer Colon
5	Normal Colon
6	Cancer Colon
7	Placental DNA Control

Figure 4B



Lane	Tissue
1	DNA Molecular Weight Marker
2	Placental DNA Control
3	Normal Colon
4	Cancer Colon
5	Normal Breast
6	Cancer Breast
7	Cancer Breast
8	BPH Prostate
9	Cancer Prostate
10	BPH Prostate
11	Normal Lung
12	Normal Lung
13	Cancer Lung

Figure 5



Lane	Tissue	Lane	Tissue
1	Kidney	8	Normal Colon
2	Bladder	9	Normal Colon
3	Prostate	10	Cancer Colon
4	Breast	11	Cancer Colon
5	Lung	12	Cancer Colon
6	Normal Colon	13	Cancer Colon
7	Normal Colon	14	Markers